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BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

Paper No. 15

Application Number: 09/553,094
Filing Date: April 18, 2000
Appellant(s): ANDERSON ET AL.

mailed date 08803

Pamela J. Sisson
For Appellant

EXAMINER'S ANSWER

This is in response to the appeal brief filed March 24, 2003.

(1) Real Party in Interest

A statement identifying the real party in interest is contained in the brief.

(2) Related Appeals and Interferences

A statement identifying the related appeals and interferences which will directly affect or be directly affected by or have a bearing on the decision in the pending appeal is contained in the brief.

(3) Status of Claims

The statement of the status of the claims contained in the brief is correct.

(4) Status of Amendments After Final

No amendment after final has been filed.

(5) Summary of Invention

The summary of invention contained in the brief is correct.

(6) Issues

The appellant's statement of the issues in the brief is correct.

(7) Grouping of Claims

The rejections of claims 1 and 8 stand or fall together because appellant's brief does not include a statement that this grouping of claims does not stand or fall together and reasons in support thereof. See 37 CFR 1.192(c)(7).

(8) Claims Appealed

The copy of the appealed claims contained in the Appendix to the brief is correct.

(9) Prior Art of Record

No prior art is relied upon by the examiner in the rejection of the claims under appeal.

(10) Grounds of Rejection

The following ground(s) of rejection are applicable to the appealed claims:

Claims 1 and 8 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific, substantial, and credible asserted utility or a well established utility.

The claimed subject matter is not supported by a specific, substantial, and credible utility because the disclosed uses are generally applicable to broad classes of this nucleic acid molecule subject matter. In addition, further characterization of the

claimed subject matter would be required to identify or reasonably confirm a "real world" use. The examiner does not find an adequate nexus between the evidence of record and the asserted properties of the claimed nucleic acid molecule subject matter.

The claims are drawn to substantially purified nucleic acid molecules that encode a maize protein or fragment thereof comprising the nucleic acid sequence of SEQ ID NO: 1.

The specification identifies SEQ ID NO. 1 as being isolated from Zea maize endosperm tissue (page 86 of the specification and the sequence listing). There is no disclosure or evidence to show that SEQ ID NO: is specific to endosperm or that its activity/expression is involved in developmental regulation or processes.

SEQ ID NO: 1 is 341 residues in length. No open reading frame, start/stop codons, or encoded protein is identified in the specification for SEQ ID NO: 1. No specific biological function is asserted for any protein encoded by SEQ ID NO: 1.

There is no other particular identifying information associated with SEQ ID NO: 1 and the specification does not list any potentially homologous prior art sequences for SEQ ID NO: 1.

General uses of polynucleotides set forth in the specification, as filed, include acquiring genes, identifying polymorphisms, determining plant traits, measuring or regulating protein expression, and DNA mapping. (See at least pages 10-15 and 33-74.) None of these is considered to be specific and substantial in view of the limited information provided in the specification. No plant traits are attributed to SEQ ID NO: 1. No complete gene is disclosed for SEQ ID NO: 1. No DNA maps or chromosomal

locations are identified. No polymorphisms are identified. The specification does not disclose how a polymorphism would be recognized by those of ordinary skill in the art given the incomplete sequences disclosed. One of ordinary skill in the art would have reason to doubt that SEQ ID NO: 1 was full length based upon the short length of the claimed SEQ ID NO. The specification does not disclose any proteins, specifically one encoded by SEQ ID NO: 1. The specification does not disclose any ORF for SEQ ID NO: 1.

Further research and experimentation would be required to identify a full length sequence that encoded a full-length protein, to characterize the chromosomal location, to determine the presence of polymorphisms, and to determine any associated plant traits. Identifying and studying the properties of the claimed subject matter itself or the mechanisms in which the claimed subject matter is involved does not define a "real world" context or use.

These uses require that the claimed nucleic acid molecule be usable as a laboratory reagent. Laboratory reagents must be sufficiently characterized and their properties understood to be used in these types of methods. In the absence of such characterization, no meaningful information is provided. The claimed nucleic acid molecule is a starting material for further research and not a research tool.

Claims 1 and 8 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a credible, specific,

and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim 1 is rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a written description rejection.

Claim 1 is directed to a nucleic acid molecule "that encodes a maize protein or fragment thereof comprising." The specification fails to describe any open reading frames, start/stop codons, or encoded proteins for SEQ ID NO: 1. As such, these nucleic acid molecules are not described. At best, the SEQ ID NO. may include a sequence encoding a fragment but not a full length protein.

The use of the term "comprising" is interpreted to encompass full length proteins and gene sequences that have not been disclosed. The common structural features of these encoded plant proteins or fragments are not disclosed and thus the claimed subject matter cannot be considered as being described.

The specification describes only the particular SEQ ID NO. and no longer sequences containing SEQ ID NO: 1. One can only envision the particular sequence disclosed and cannot envision any encoded protein sequence or larger sequences in which the claimed SEQ ID NO. is embedded.

Further, while the specification discloses that SEQ ID NO: 1 is isolated from maize, the specification does not disclose that SEQ ID NO: 1 is specific to maize. The

specification discloses that proteins encode by inventive sequences may be homologous to those from other organisms (see pages 20-21), wherein a homologous protein may be 100% identical to a protein encoded by an inventive sequence. Thus, the specification teaches that an inventive nucleotide sequence may encode a protein found in a variety of organisms. SEQ ID NO: 1, although obtained from a maize library, may encode a non-maize protein. The instant specification fails to teach that SEQ ID NO: 1 is known to encode any protein, particularly one which is specific to maize.

11) Response to Argument

Appellant's arguments are addressed *seriatum*.

Sections 2A and 2B

Appellants assert that the claimed invention meets the utility and enablement requirements because they have disclosed a "nucleic acid molecule which, in its current form, provides at least one specific benefit to the public, *e.g.*, the ability to identify the presence or absence of a polymorphism in a population of corn plants." The examiner does not agree that the claimed nucleic acid molecule provides any specific benefit to the public in its current form but rather requires further experimentation to determine whether such a benefit can be found. Appellants also assert that the specification has provided an adequate description for a nucleic acid molecule "comprising" or "that encodes" a maize protein or fragment thereof comprising" the sequence of SEQ ID NO: 1 because they have disclosed SEQ ID NO: 1. The examiner does not agree that the structure of SEQ ID NO: 1 provides adequate description for claims encompassing the

nucleic acid for the gene or encoding full length proteins. Neither the structural and functional properties of any gene (including introns and other non-coding sequence) comprising SEQ ID NO: 1 nor the structural and functional properties of any protein or fragment thereof encoded by a nucleotide sequence comprising SEQ ID NO: 1 is disclosed in the specification.

The Examiner agrees that the "the basic quid pro quo...for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility...where specific utility exists in currently available form." Whether the instant application has met this burden is the subject of this appeal.

The brief does not dispute that no open reading frame (ORF), no encoded protein, nor any biological activity for any encoded protein has been disclosed for SEQ ID NO: 1.

Appellant argues that the claimed nucleic acid molecules can be used as hybridization probes for expression profiling, as antisense inhibitors by introduction of the claimed nucleic acid molecules into a plant or plant cell where the resulting cell or plant is to be used to screen compounds, to measure the level of mRNA in a sample, and as a molecular marker. The Examiner maintains that further research is required for such uses.

Appellant argues that they have "proven" that the claimed nucleic acid molecule can be used to detect the presence or absence of a polymorphism in a population of corn plants. The specification generally teaches using the claimed polynucleotides to identify a polymorphism, but fails to teach that a polymorphism could in fact be

detected, or a specific polymorphism that could be detected. The specification generally teaches using a polymorphism, detectable with the claimed nucleic acid molecules, as a molecular marker for a linked trait of interest, but fails to teach either the polymorphism or the trait of interest. The court in *Kirk* (at page 53) held:

> **We do not believe that it was the intention of the statutes to require the Patent Office, the courts, or the public to play the sort of guessing game that might be involved if an applicant could satisfy the requirements of the statutes by indicating the usefulness of a claimed compound in terms of possible use so general as to be meaningless and then, after his research or that of his competitors has definitely ascertained an actual use for the compound, adducing evidence intended to show that a particular specific use would have been obvious to men skilled in the particular art to which this use relates.**

The specification (page 39, line 17) defines "polymorphism" as "a variation or difference in the sequence of the gene or its flanking regions that arises in some members of a species" (emphasis added). The following pages of the specification discuss various types of sequence polymorphisms and how they are detected. It is noted that on page 42, line 22, the specification states, "By correlating the presence or absence of it [a polymorphism] in a plant with the presence or absence of a phenotype..." and on page 46, line 3, the specification states "Polymorphisms are useful, through linkage analysis..." Thus, the specification acknowledges that further

analysis is required to determine a use for a polymorphism even assuming one is found. A change of phenotype and correlation with phenotype must be found; linkage analysis must be performed.

Even to determine whether a polymorphism exists at a specific chromosomal location requires hybridization to at least two individual chromosomes, and generally involves analyzing genomic DNA from multiple members of a species; the specification discloses no such analysis. The specification fails to disclose: 1) whether the claimed nucleic acid molecule can in fact detect a polymorphism, or even whether such a polymorphism exists; and 2) at least one specific example of at least one of the types of polymorphisms described in the specification. The specification does not disclose any utility in this context for a nucleic acid molecule or EST that can NOT detect a polymorphism. Therefore, using the claimed invention to first determine whether or not the claimed nucleic acid molecule can, in fact, detect a polymorphism *is* to determine whether or not the claimed invention has a utility that requires detecting a polymorphism, i.e. it is "use testing" and not substantial. Since the specification fails to identify even one specific polymorphism that can be detected with the claimed nucleic acid molecule, the specification fails to show any specific correspondence between the disclosed general utility and the claimed subject matter, regardless of any specific application requiring detection of polymorphisms.

Appellants argue that the claimed nucleic acid molecules have utility in "isolating specific promoter sequences, and to obtain nucleic acid homologues." The argument in the brief compares the claimed invention to a microscope.

nucleic acids in maize, so does it fail to describe a specific and substantial utility for any corresponding nucleic acids in other plant species.

The brief on page 8 discusses gas chromatographs. MPEP 2107 in discussing research tools sets forth the following:

> ***Some confusion can result when one attempts to label certain types of inventions as not being capable of having a specific and substantial utility based on the setting in which the invention is to be used. One example is inventions to be used in a research or laboratory setting. Many research tools such as gas chromatographs, screening assays, and nucleotide sequencing techniques have a clear, specific and unquestionable utility (e.g., they are useful in analyzing compounds). An assessment that focuses on whether an invention is useful only in a research setting thus does not address whether the invention is in fact "useful" in a patent sense. Instead, Office personnel must distinguish between inventions that have a specifically identified substantial utility and inventions whose asserted utility requires further research to identify or reasonably confirm. Labels such as "research tool," "intermediate" or "for research purposes" are not helpful in determining if an applicant has identified a specific and substantial utility for the invention.***

Again, further experimentation is required to use determine and confirm any of the uses set forth by appellant for the claimed nucleotide sequences.

The gas chromatograph example set forth by appellant, particularly as discussed in Footnote 3 on page 9, is not analogous to the present disclosure. A gas

A microscope is useful for determining structure of *any* sample of interest at the macroscopic, microscopic or molecular level, depending on the type of microscope. It is a generally useful tool for a wide range of specific uses. One does not usually use a microscope to study related microscopes. In contrast, Appellant argues that the claimed nucleic acid molecules are useful to detect or measure nucleic acid molecules that possess a certain level of structural relatedness to the claimed nucleic acid molecules, the level of relatedness being defined by hybridization to the claimed nucleic acid molecules. However, the specification discloses *no* nucleic acid molecule that hybridizes with the claimed nucleic acid molecules that does *not* consist or comprise SEQ ID NO: 1 or its complement. In order for hybridization between two nucleic acid molecules to occur, they must share at least some nucleotide sequence that is fully complementary. The length of fully complementary sequence required to detect hybridization depends primarily on the stringency of the specific hybridization conditions employed, the lower the stringency the shorter the length of fully complementary sequence required. The specification also fails to disclose any hybridization conditions required for detecting nucleic acid molecules that do *not* contain the nucleotide sequence of SEQ ID NO: 1 or its complement, in addition to failing to disclose any source for such nucleic acid molecules.

All arguments pertaining to the utility of the claimed invention with respect to studying the corresponding genomic DNA and mRNA found in maize, would also apply to any homologous nucleic acid molecules found in other plant species. In so much as the specification fails to describe a specific and substantial utility for corresponding

chromatograph is a piece of equipment designed and built for a particular use. Such equipment is fully tested, evaluated, and calibrated to ensure accurate results. Those skilled in the art use gas chromatographs to analyze both known and unknown compounds. When the compound is unknown, the results obtained are compared to results for known compounds, e.g. standards. Appellants did not design the claimed nucleotide sequences for any particular purpose. They merely isolated them. They have not tested, evaluated, or calibrated the claimed nucleotide sequences for any particular use. Sampling for the presence or absence of chlorine in a crude oil sample is not analogous to the present situation. The presence or absence of chlorine in a crude oil sample has a known meaning based upon prior research. Absent establishment of this association between presence of chlorine and destruction of catalyst, the presence or absence of chlorine in a sample would not provide any useful information to the refinery manager. Likewise, the presence or absence of any of the claimed nucleotide sequences in a sample (or polymorphisms thereof) has no meaning absent some association. Further experimentation is required to determine what that meaning or association might be.

In addition, this gas chromatograph analogy fails address Appellants' own definition of the term polymorphism. The specification (page 39, line 17) defines "polymorphism" as "a variation or difference in the sequence of the gene or its flanking regions that arises in some members of a species." It follows from this definition that if there is no "variation or difference in the sequence of the gene or its flanking regions" among "members of a species," then no polymorphism exists, i.e. a polymorphism is

absent, in this region of the genome. A "polymorphism" is a collective concept defined by at least two variants (or alleles) found within members of a species collectively. Thus, one detects the *presence* of a polymorphism by analyzing multiple members of the species, i.e. analyzing a population. While one can detect the absence (or presence) of a specific allele of the polymorphism in a specific individual member of the species, one cannot detect the *absence* of a polymorphism *per se* based on one individual alone. The absence of a particular allele necessarily means that a different allele is present. The specification fails to disclose a specific and substantial utility for the claimed invention in the capacity of detecting polymorphisms, because it does not disclose whether the claimed nucleic acid molecules can, in fact, be used to detect any polymorphism whatsoever. Thus, the specification leaves open the possibility that there may be no polymorphism to detect. With respect to the gas chromatograph analogy, one can only detect the absence of a compound, such as chlorine, in a sample, *if* it was already known that chlorine could, in fact, be detected by the gas chromatograph were it present in the sample.

Appellants cite *Carl Zeiss Stiftung v. Renishaw PLC* in support of their position that utility has been established. However, this decision is with respect to a mechanical device and not a laboratory reagent or research tool. Furthermore, applicant mischaracterizes the findings in this decision. This decision concerned claim interpretation and the CAFC found that the district court had erred in their interpretation of what the claim embraced and thus what was required to establish utility. The claimed

device was found to fulfill the stated objective of mounting a stylus by the CAFC. These facts do not correspond to the instant specification

While the specification teaches (page 35, line 4) that the claimed nucleic acid molecules "*may be employed* to obtain other nucleic acid molecules" (emphasis added), the specification does not indicate that any such nucleic acid molecules *had been* obtained, nor does it describe any characteristics possessed by such nucleic acid molecules. As to whether such molecules could, in fact, be obtained, the Office can neither prove nor disprove the assertion because the Office does not have laboratory facilities. At the time the application had been filed, future experimentation on the part of one skilled in the art would have been required to determine which, if any, other plant species contained nucleic acid molecules that could have been obtained using the claimed invention, and under what experimental conditions.

In the context of "identifying a unique subset of related sequences", the claimed invention does not compare to a golf club, because one knows what a golf ball is and how to use the golf club to hit it, whereas the specification does not disclose or describe with particularity any known useful nucleic acid molecule that can be obtained (i.e. a "related sequence"), - it simply invites the skilled artisan to provide such information by further experimentation.

Substantial utility means that "one skilled in the art can use a claimed discovery in a manner which provides some *immediate* benefit to the public," *Nelson v. Bowler*, 206 USPQ2d 881, 883 (CCPA 1980) (emphasis added). Since the specification does not describe any other specific nucleic acid molecule, sufficient to inform one skilled in

the art that it has been isolated, there can be no "*immediate* benefit to the public" in using the claimed nucleic acid molecule in this capacity; "a patent is not a hunting license. It is not a reward for the search, but compensation for its successful conclusion," *Brenner* at page 696.

The brief states in Footnote 1 on page 5 that "the examiner's sole reliance" on the Interim Guidelines (Federal Register Vol. 63, No. 114) is improper as the Interim Guidelines "do not have the force and effect of law." The rejection of claims 1 and 8 is made under 35 USC 101, and thus is properly made under the law. The Interim Guidelines were cited in a previous Office Action merely to provide a definition for the terms "specific, substantial, and credible" as applied under the statute. At least the terms "substantial utility" and "specific benefit" are used in the *Brenner v. Manson* decision quoted on page 3 of the Appeal Brief. *Nelson v. Bowler*, 206 USPQ2d 881, 883 (CCPA 1980) defined "substantial utility" to mean that "one skilled in the art can use a claimed discovery in a manner which provides some *immediate* benefit to the public," (emphasis added). Thus, whether a utility is at least "specific" and "substantial" is clearly a matter for consideration when analyzing claimed subject matter for compliance with the requirements of 35 USC 101.

With respect to credibility, appellant is reminded that in order to meet the requirements of 35 USC 101, the specification must disclose at least one utility that is specific and substantial, as well as credible (absent a showing of well established utility, which would presume that the utility was credible). The claims have been rejected because 1) the specification fails to disclose at least one utility that is both specific and

substantial, and 2) no convincing evidence has been presented to show that an EST, for which only its nucleotide sequence and source have been disclosed, has a well established utility.

Section 2C

The Examiner maintains that the uses asserted for the claimed invention are methods where the claimed invention is, itself, an object of scientific study, e.g. to determine whether the corresponding genomic DNA of maize contains a polymorphism that can be detected with the claimed invention. The specification cannot enable or tell how to use the invention within 35 U.S.C. 112, first paragraph, if there is no patentable utility within 35 U.S.C. 101. The Examiner maintains that there is no patentable utility for the claimed invention for the reasons set forth above and thus the claims are not enabled.

Section 2D

The issue is whether Applicant was in possession of the genus being claimed. This genus is not restricted to any particular disclosed subgenus or species, such as vectors comprising SEQ ID NO: 1 as an insert. The only nucleic acid molecule described by complete structure is that consisting of SEQ ID NO: 1. The only nucleic acid molecules comprising SEQ ID NO: 1 described in the specification by other characteristics are generic vectors. While it is acknowledged that Appellant need not describe "every nuance" of the claimed invention, the written description must bear a

reasonable correlation to that which is claimed. The disclosed subgenus and species embraced by the claim is not representative of the entire genus being claimed. The genus of nucleic acid molecules being claimed embraces any and every type of nucleic acid molecule that comprises SEQ ID NO: 1 and additional sequences of any size and sequence, not just vector backbones. Clearly, at the time of filing, Appellant was not in possession of genomic materials that contain the common EST fragment, which are embraced by the open-ended claims. The specification does not disclose what characteristics these additional sequences may or may not have that are consistent with the operability of the nucleic acid molecules as probes or primers for detection of SEQ ID NO: 1 in a target sequence, and all disclosed uses for the claimed nucleic acid molecule is fundamentally as a probe or primer, at least in some aspect. The specification does not disclose encoding sequences or open reading frames (ORFs).

With respect to full length mRNAs, cDNAs and genomic sequences, one skilled in the art would reasonably conclude that the claim embraces these nucleic acid molecules, and the specification provides no physical (i.e. structural) characteristics of these molecules to distinguish them from other nucleic acid molecules comprising SEQ ID NO: 1, and no other indication that would suggest Appellant possessed them. This particular subgenus embraced by the claims has a disclosed potential utility not possessed by those members of the claimed genus useful only in hybridization. Full length mRNAs, cDNAs and genomic sequences (genes) would encode the corresponding protein(s).

A fundamental issue here is specific to the very narrow class of product that is nucleic acid molecules. The basic question upon which Appellants and the Examiner disagree is whether the disclosure of a partial sequence of otherwise uncharacterized nucleic acid molecules that may encode a corresponding protein is sufficient to establish possession of a broad genus based solely on the description of the partial sequence, where the broad genus embraces the uncharacterized nucleic acid molecules by default. The subgenus of uncharacterized nucleic acid molecules that encode any corresponding protein is explicitly alluded to in the specification, and disclosed as possessing an additional use *not* possessed by any other members of the broad genus being claimed, i.e. encoding the protein. The specification fails to provide any structural or functional characteristic for these desired nucleic acid molecules, which encode the protein, that would distinguish them from the other members of the genus, which simply comprises SEQ ID NO: 1 as the sole distinguishing feature.

That Appellants' claim embraces nucleic acid molecules that encode a corresponding protein, whatever it may be, is clearly evident from the claim language chosen. The only species of nucleic acid specifically enumerated is the nucleic acid molecule of SEQ ID NO: I itself. The specific embodiments that in addition to SEQ ID NO: 1 include nucleic acids that will allow the corresponding protein to be encoded cannot be predicted without the coding sequence itself. This coding sequence has not been disclosed. Clearly, the specification would not show one skilled in the art that

these desired subcombinations were possessed by Appellant, and thus the embracing genus was also not possessed.

For the above reasons, it is believed that the rejections should be sustained.

Respectfully submitted,

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